ABSTRACT

Quantitative methods for analyzing measurement errors from nucleic acid
arrays are provided. The methods are based on a two component model that
approximates a constant standard deviation for very low expression levels, and
constant relative standard deviation (RSD) for higher concentrations. Estimates of
some model parameters may be obtained without resort to replicated measurements.
Also provided are thresholding methods for establishing boundaries between low
expression levels, high expression levels, and intermediate expression levels, and
methods for estimating actual expression levels from intensity measurements.